

Nucleotide Sequence

|      |             |             |             |             |             |             |            |             |      |
|------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|------|
| 1    | GGACGTCGAG  | GCATTACAT   | CGCGAACCA   | AGCCATAGCA  | TGAAACAGCG  | AGCTTCAGC   | CTCACCGACG | AGTCTCACT   | 80   |
| 81   | AAAAGGACT   | CCCGAGCTA   | GGGTGGGA    | CTCGGCTCA   | CACAGTAGT   | GCCGGCTATT  | GGACTTTTGT | CCAGTGACAG  | 160  |
| 161  | CTGAGACAC   | AAGGACCAG   | GGAGAGGTG   | TAGGAGAGAA  | GCGCCGCGA   | CAGCGATCG   | CCAGCACCA  | GTCCGCTCC   | 240  |
| 241  | AGGCTTTCGG  | TTTCTTTGG   | TCCATCTTG   | GTGCGCCTTC  | CCGGCGTCTA  | GGGAGCGGA   | GGCTGAGTG  | GCAGCGGCG   | 320  |
| 321  | GAGAGTCCG   | CCGCGACAG   | ACGAATCCC   | CCACTGGAAA  | GGNTTCTGNA  | AGAAATGAG   | TCAGCCCTCA | GAAATGAGT   | 400  |
| 401  | TGACTGCCCTG | CTGGCTTCC   | TGTTGACTGG  | CCCGGAGCTG  | TACTGCAAGA  | CCCCTGTGAG  | CTTCCCTAGT | CTAAGAGTAG  | 480  |
| 481  | GATGCTGCT   | GAAGTCATCC  | ATCAGGTTGA  | AGAGGCACTT  | GATACAGATG  | AGAAAGGAGT  | GCTGCTCTTT | TTGTGCCGGG  | 560  |
| 561  | ATGTTGCTAT  | AGATGTGGT   | CCACCTAATG  | TCAGGGACCT  | TCTGGAATAT  | TTACGGGGA   | GAGGTAGCT  | GTCTGTGGG   | 640  |
| 641  | GACTTGGCTG  | AACTGCTCTA  | CAGAGTGAGG  | CGATTGACC   | TGCTCAACG   | TATCTTGAG   | ATGGACAGAA | AAAGCTGTGA  | 720  |
| 721  | GAACCCACTG  | CTCAGGAAC   | CTCACCTTGT  | TTCCGACTAT  | AGAGTGTCTA  | TGGCAGAGT   | TGGTGAAGT  | TTGGTAAAT   | 800  |
| 801  | CTGATGTGTC  | CTCATTAAAT  | TTCTCATGA   | AGGTTACAT   | GGCCGAGGC   | AAAGTAAGCA  | AGGAGNAGAG | TTTCTTGGAC  | 880  |
| 881  | CTTGTGGTGG  | AGTTGGAGAA  | ACTAATTTG   | GTGCCCCAG   | ATCAACTGA   | TTTATTAGAA  | AAATGCCATA | AGMACATCCA  | 960  |
| 961  | CAGANTAGAC  | CTGAGACMA   | AAATCCAGNA  | GTACAAAGCAG | TCTGTTCNAG  | GAGCAGGGAC  | AAATTAACAG | AAATTTCTCC  | 1040 |
| 1041 | AAGCAGCAAT  | CCAAAGAGT   | CTCAAGGATC  | CTTCANATA   | CTTCAGGCTC  | CATTAATGGA  | GAAGTAAGA  | ACAAAGACTT  | 1120 |
| 1121 | AGGACAGAC   | TTGGCGCTCA  | ACAAAGACCA  | GTGAAAGAAAT | CCATTACAG   | ATCAGAAAGCT | TTTTCGCTC  | AGAGCATACC  | 1200 |
| 1201 | TGAAAGAGAG  | TACNAGNTGA  | AGAGCAAGCC  | CCTAAGGAATC | TGCTGTGATA  | TCGNTTGCAT  | TGGCAATGAG | ACAGAGCTTC  | 1280 |
| 1281 | TTGAGACAC   | CTTCACTTCC  | CTGGGCTATG  | AAATCCAGNA  | ATTTCTTGCAT | CTCAGTATGC  | ATGGTATATC | CCAGNTTCTT  | 1360 |
| 1361 | GGCCAAATTG  | CCTGATGCC   | CGAGCACCGA  | GACTACGACA  | GCCTTGTGTG  | TGTCCTGGTG  | AGCCGAGGAG | GCCTCCAGAG  | 1440 |
| 1441 | TGTGTATGGT  | GTGGATCAGA  | CTCACTCAGG  | GCCTCCCTTG  | CATCACTATCA | GGAGGATGTT  | CATGGGAGAT | TCTATGCCCTT | 1520 |
| 1521 | ATCTAGCAGG  | GAAGCCAAAG  | ATGTTTCTTA  | TTCAAGAACTA | TGTGGTGTCA  | GAGGGCCAGC  | TGGAGAACAG | CAGCCTCTTG  | 1600 |
| 1601 | GAGGTGGATG  | GGCCAGCGNT  | GAAGAAATGTG | GAATTCMAAG  | CTCAGAAAGC  | AGGGCTGTGC  | ACAGTTCACC | GAGAAAGCTGA | 1680 |
| 1681 | CTTCTTCTGG  | AGCCTGTGTA  | CTGGGACAT   | GTCCCTGCTG  | GAGCAGTCTC  | ACAGCTCACC  | GTCCCTGTAC | CTGCAAGTGGC | 1760 |
| 1761 | TCTCCCAAG   | ACTGAGACMA  | GAAGAAAC    | GCCCACTCCT  | GGATCTTAC   | ATTGAACTCA  | ATGGCTACAT | GTATGATGG   | 1840 |
| 1841 | AACAGCAGAG  | TTTCTGCCMA  | GGAGAAATAT  | TATGTCTGGC  | TGCAGACAC   | CTGAGAAAG   | AACTTATACC | TCTCCTACAC  | 1920 |
| 1921 | AAAGAAACC   | AAAGGCTGG   | GCCTAGTGGC  | TCACACCTGT  | AAATCCAGCA  | CTTTGGGAGG  | CCAAAGAGGG | CAGATCACTT  | 2000 |
| 2001 | CAGGTACAG   | GTTCGAGACC  | AGCCTGGCCA  | ACATGGHAA   | CGCTGTCCCT  | AGTAANAATG  | CAAAATATAG | CTGGGTGTGG  | 2080 |
| 2081 | GTGTGGGTAC  | CTGTGTTCCC  | AGTTACTTGG  | GAGGCTGAGG  | TGGGAGGATC  | TTTGAACCC   | AGGAGTTCAG | GGTCNTAGCA  | 2160 |
| 2161 | TGCTGTGATT  | GTGCCCTACGA | ATAGCCACTG  | CATACCAACC  | TGGGCAATAT  | AGCAAGNTCC  | CATCTCTTAA | AAAAAANA    | 2240 |
| 2241 | AAA         |             |             |             |             |             |            |             | 2243 |

FIG. 1A

2/11

Deduced Amino Acid Sequence

MSAEVHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRKAVE  
 THLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLVVELEKLNLVAPDQDLLEKCLKNIIH  
 RIDLTKIQKYKQSVQGAGTSYRNVLAQAIQKSLKDPNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQSEAFLPQSIP  
 EERYKMKSKPLGICLIIDCIGNETELLRDFTTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCLVSRGGSQS  
 VYGVDDQTHSGCLPLHHIRRMFMGDSCPYLAGPKMFFIQNYVVSSEGQLENSLLEVDGPAMKNVEFKAQKRGCLCTVHREAD  
 FFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWSRVSAKEKYVWLQHTLRKKLILSYT

2.

FIG. 1B

Nucleotide Sequence

|      |            |             |             |             |             |              |             |             |      |
|------|------------|-------------|-------------|-------------|-------------|--------------|-------------|-------------|------|
| 1    | GGACGTCGAG | GCATTACAAAT | CGCGAATACCA | AGCCATAGCA  | TGNAACAGCG  | AGCTTGCAGC   | CTCACCAGCG  | AGTCTCAACT  | 80   |
| 81   | AAAAGGACT  | CCCGAGCTA   | GGGTGGGA    | CTCGGCTCA   | CACAGTGAAT  | GCCGGCTAAT   | GGACTTTTGT  | CCAGTGACAG  | 160  |
| 161  | CTGAGACAC  | AAGGACCAAG  | GGAGGAGTG   | TAGGAGAGAA  | GCGCCGCGNA  | CAGCGATCGC   | CCAGCACCA   | GTCCGCTTCC  | 240  |
| 241  | AGGCTTTGG  | TTTCTTTGG   | TCCATCTTGG  | GTCCGCTTTC  | CAGGCTCTA   | GGGAGCGAA    | GGCTGAGGTG  | GCAGCGGCAG  | 320  |
| 321  | GAGAGTCCG  | CCCGACAGG   | ACGAACTCC   | CCACTGGA    | GGATCTGNA   | AGAAATGAAG   | TCAGCCCTCA  | GAATGAAGT   | 400  |
| 401  | TGACTGCTG  | CTGGCTTCC   | TGTTGACTG   | CCCGAGCTG   | TACTGCAAGA  | CCCTTGTGAG   | CTTCCCCTAGT | CTAAGAGTAG  | 480  |
| 481  | GATGCTGCT  | GAAATCATCC  | ATCAGGTTGA  | AGAAACACTT  | GATACAGATG  | AGAGGAGAT    | GCTGCTCTTT  | TTGTGCCGGG  | 560  |
| 561  | ATGTTGCTAT | AGATGTGGTT  | CCACCTAATG  | TCAGGACCT   | TCTGGATAT   | TTACGGGAAA   | GAGGTAACT   | GTCTGTCGGG  | 640  |
| 641  | GACTTGGCTG | AACTGCTCTA  | CAGAGTGAGG  | CGATTTGACC  | TGCTCAACCG  | TATCTTGAAG   | ATGGACAGAA  | AAGCTGTGGA  | 720  |
| 721  | GACCCACCTG | CTCAGGAAAC  | CTCAGCTTGT  | TTCCGACTAT  | AGAGTGTGA   | TGGCAGAGAT   | TGGTGAGGAT  | TTGGATAAAT  | 800  |
| 801  | CTGATGTGTC | CTCATTAAT   | TTCTCTCATG  | AGGATTAAT   | GGCCCGAGGC  | AGATTAAGCA   | AGGAGAAAG   | TTTCTTGGAC  | 880  |
| 881  | CTTGTGGTTG | AGTTGGAGAA  | ACTAATTTG   | GTTGCCCCAG  | ATCAACTGGA  | TTTATTAAGAA  | AAATGCCCTAA | AGAAATCCA   | 960  |
| 961  | CAGAAATAG  | CTGAAGACAA  | AAATCCAGAA  | GTACAAAGCAG | TCTGTCTCAAG | GAGCAGGGAC   | AGATTACAGG  | AATGTTCTCC  | 1040 |
| 1041 | AGCAGCAAT  | CCAAAGAGT   | CTCAAGGATC  | CTTCAATTA   | CTTCAGGATG  | ATAACACCTT   | ATGCCCATTTG | TCCATGATCTG | 1120 |
| 1121 | AAATTCCTG  | GAAATTTCTC  | CATGAGATTA  | ACNTGGAAT   | GCCTCTACTT  | AAATCATTTCTG | AATGATTA    | TGGTTTCAAT  | 1200 |
| 1201 | TTCTAAATGT | GTATATAATGT | GTTAAGCCCT  | TTCTTTGTC   | TGTATGTTTA  | GATGCTTTCC   | AATCTTTTGT  | TACTACTAAT  | 1280 |
| 1281 | AATGCTATAA | AATAAATATC  | CTTGACTTTC  | TTTAAATAA   | AAAAA       | AAAAA        | AAAAA       | AAAAA       | 1360 |
| 1361 | AAAAAAAAAA | AAA         |             |             |             |              |             |             | 1373 |

Deduced Amino Acid Sequence

MSAEVHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERGLSVGDIAELLYRVRFDLLKRLKMDRKAVE  
 THLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMRGKISKESKSFLLVVELEKLNVLNVPDQLDLLEKCLKNIII  
 RIDLTKIQKYKQSVQAGTSYRNVLQAAIQSLKDPNNFRMTTPYAHCPDLKILNCMSMZ

FIG. 2

**SECRET**

**1st DED module**

|  |      |             |    |
|--|------|-------------|----|
| MAQSPVSAEVIHQVEICLDEDEKENMLFLCROVITENLAAPNVR                   | DLDS | LSERQQLSFAT | 86 |
| MSAEVIHQVEEALDTDEKENMLFLCROVA                                  | DLDP | LREKQLSVGD  | 81 |
| MSAEVIHQVEEALDTDEKENMLFLCROVA                                  | DLDP | LREKQLSVGD  | 61 |
| MDFSRLNYDIGEQLDSEDLASLKEFLSLDYLPORKQEPKDALMLFORLOEKRM          | DLDS | LSERQQLSFAT | 68 |
| MKSQGHWYSSDXNCKVSRFKLLIIDSNLGVODVENLKEFLCIGLYPNKKLEKSSASQVFEHL | DLDS | LSERQQLSFAT | 84 |

**2nd DED module**

|      |    |    |    |      |      |     |     |     |     |    |    |    |    |    |    |    |    |     |      |    |    |    |    |    |    |    |     |    |    |    |    |    |    |     |     |      |     |     |
|------|----|----|----|------|------|-----|-----|-----|-----|----|----|----|----|----|----|----|----|-----|------|----|----|----|----|----|----|----|-----|----|----|----|----|----|----|-----|-----|------|-----|-----|
| VRRF | DL | KR | LR | KT   | DKA  | TV  | EDH | LRN | PHL | VS | DR | VR | VL | ME | IG | ES | LD | QND | VSS  | LV | FL | TR | DR | VT | GR | GK | JAK | DK | KS | FF | LD | LV | I  | ELE | EK  | LN   | 150 |     |
| VRRF | DL | KR | LR | KMDR | KAVE | TH  | LL  | LRN | PHL | VS | DR | VR | VL | MA | EE | IG | ED | DKS | DVSS | LV | FL | TR | MK | DD | YM | GR | GK  | IS | KE | KS | FF | LD | LV | I   | ELE | EK   | LN  | 142 |
| VRRF | DL | KR | LR | KMOR | KAVE | TH  | LL  | LRN | PHL | VS | DR | VR | VL | MA | EE | IG | ED | DKS | DVSS | LV | FL | TR | MK | DD | YM | GR | GK  | IS | KE | KS | FF | LD | LV | I   | ELE | EK   | LN  | 142 |
| YNRL | DL | LY | LN | TR   | KEE  | ME  | REL | QTP | RAQ | IS | AL | VR | VL | QI | SE | EV | SR | SE  | URS  | FK | FL | TR | DO | EE | IS | CK | DD  | DD | MM | LD | DI | IF | IS | ME  | KRV | 150  |     |     |
| IRQK | XL | QL | HL | NCT  | KEE  | VER | LL  | PT  | RQR | VS | LR | FL | BN | LL | LY | EL | SE | IG  | DS   | EN | UK | DM | FL | TR | DK | DL | SL  | PK | EL | EL | EM | TS | LS | FL  | A   | FILE | KQ  | 160 |

FIG. 3A

**060546 J. E. B.**

mCASHα QSSQGA-RSNMNTLQASLPK--LSLKYNRSRLQNGRSKEPRFVEYRDSQRTL VKTS 232  
 mCASHβ QSVQAGTGYRNVLQAAIQKSLKDPSSNNFRMITPYAHCPDLKILGNCSM\* 222  
 mCASHα QSVQAGTGYRNVLQAAIQKSLKDPSSNNFRLHNGRSKEQRLKPOLGAQOQEPVKKS 227  
 CASP-8 EE.....FSKERSSLEQS-PDE.....FSNGEELCGVMTISDSPREQD 218  
 CASP-10 REKAIQIVTP-PVD.....KEAESYQGEEELVSQTDVKVTF 223  
 CASP-1 ...QGVLSSFFAPQAVQDNPAMPTSSGSEGNVVKLCSLEEAQ 142  
 → p20

|      |       |           |       |      |      |     |        |       |     |      |    |    |    |     |     |     |   |      |     |     |
|------|-------|-----------|-------|------|------|-----|--------|-------|-----|------|----|----|----|-----|-----|-----|---|------|-----|-----|
| IOE  | SGAFL | PPHIREET  | YRMQS | ...  | KPLG | CL  | IC     | IGNDT | ... | KYLQ | ET | FT | SL | GYH | IQ  | FL  | F | PKSH | 292 |     |
| IOE  | SEAF  | LQSIPEERY | KMKs  | ...  | KPLG | CL  | IC     | IGNET | ... | EL   | RO | FT | SL | GYE | VQ  | K   | F | L    | SMH | 287 |
| S    | ES    | ...       | QTL   | DKVQ | MKS  | ... | KPRG   | YCL   | IN  | HN   | F  | A  | K  | A   | R   | E   | K | V    | P   | 289 |
| L    | E     | A         | ...   | L    | P    | R   | A      | A     | V   | Y    | R  | M  | N  | R   | ... | N   | H | R    | G   | 287 |
| ...  | SG    | ...       | I     | S    | L    | D   | N      | S     | Y   | K    | M  | D  | Y  | ... | P   | E   | M | G    | ... | 92  |
| RIWK | ...   | QKSAE     | IY    | P    | I    | M   | DKSSRT | RLAL  | IC  | N    | E  | E  | F  | D   | S   | ... | I | P    | R   | 207 |

FIG. 3B

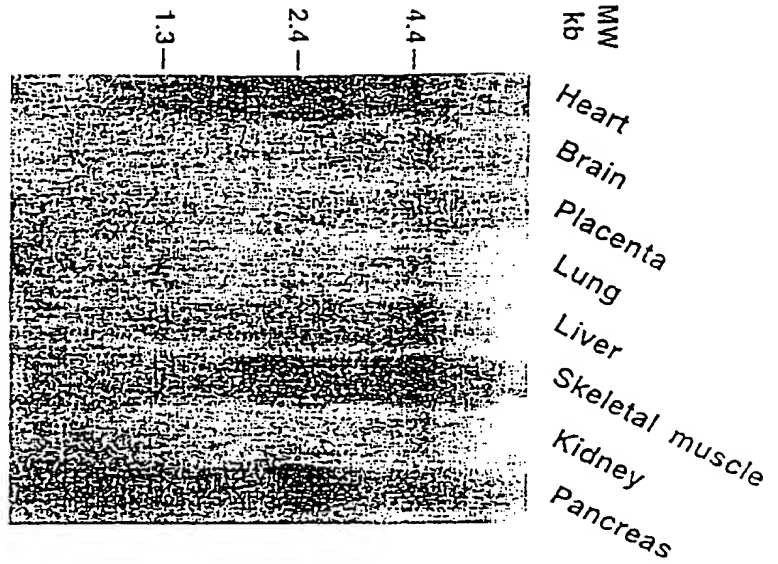
6627-2450860

mCASHa DITQIVRRYASMAQ-HQDYDSFAVCVLVSLGSGSQSMGRD.....QVHSGFSLQHVKNMFTGDTCPSLRGKPKLFFIQNYESLGS 370  
 hCASHa GISQILGQFACMPE-HRDYDSFVCLVSRGSGSQSVYGVQD.....QTHSGPLLHHIRRMFMGDSCPVLAGKPKMFFIQNYVVSSEG 385  
 CASP-8 EQIYEIWKIYQLMD-HSNMDQFICGILSHGDKGIIYGTID.....GQEG..PIYELTSOFTGLKCPSLAGKPKVFFIQACQGN- 364  
 CASP-10 EMEVLQKQKCNPA-HADGDQFVFCILTHGRFGAVYSSD.....EALI..PIREIMSHFIALQCPRLAEKPKLFFIQACQGEE- 362  
 CASP-3 EEIVELMRDVSKEH-HSKRSSFVCLVSHGEEGIIIFGTN.....G.PV..DLKKIITNFERGDRCRSLTGKPKLFFIQACRGTE- 168  
 CASP-1 SDMTTELEAFARPEH-KTSDSTFLVFMESHGIREGICGKKHSEQVPD..IL..QLNALIFNMLNTKNCPSLKDKPKVILIQACRGDS- 288  
 mCASHa QLEDSS-LEVID.....GPSIKNVDSKPLQPRHCTTHPEADILFWSLCTADVSHLEKPSSSSSSVYLQKLSQQLKQGRRRP 442  
 hCASHa QLENSLLEVID.....GPAMKNVEFKAQKRGQLCTVHREADFFFWSLCTADMSLEQSHSPSLILYLLQCLSQKLRQERKRP 438  
 CASP-8 -YQKGIPIVETID.....SEEQPYLEMDLSSPQTRYIPOEADFFLLGMATVNNCVSYRNPAEETWYIQSLCQSLRERCPR- 435  
 CASP-10 -IQPSVSIETID.....ALNPEQAPTSLODS...IPAEDFFLLGLATVPGYVSFRHVEEGSMYIQSLCNHLKKLVPR- 429  
 CASP-3 ...LDCGIEITID.....SG...VDDDMACHK...IPVEADFFLYAYSITAPGYYSWRNSKDGSWFIQSLCAMLKQYADK- 227  
 CASP-1 ...PGVVWFKEIDSVGVSGNLSLPTTE...EFEDQAIKK...AHIEKDFIAFCSTPDNVSWRHPMTMGSVFIQSLCAHMQEYACS- 381  
 mCASHa LVDLHVEL-MDKVYAWNSGVSSK.....EKYSLSLQ-HTLRKKLLI LAPT\* 486  
 hCASHa LLDLHIELNGY-MYDWNRSRVSAK.....EKYYVWLQ-HTLRKKLLI LSYT\* 481  
 CASP-8 GDDILTILITEV-NYEVSNKDDKK.....NMGKQMPQPT-FILRRKKLVFPSPD\* 479  
 CASP-10 HEDILSILITAV-NDDVSRRVDKQ.....GTTKQMPQPA-FILRRKKLVFPVPLDALS! 480  
 CASP-3 -LEFMHILITRV-NRKVATEFESFSFDFHAKKQIIPGIV-SMLTKELIYFYH\* 277  
 CASP-1 -CDIVEEILFRKVI-RFSFEQ-PD.....GRAQMPITERTVITLTRCFYLFPGH\* 404

FIG. 3C

7/11

A



B

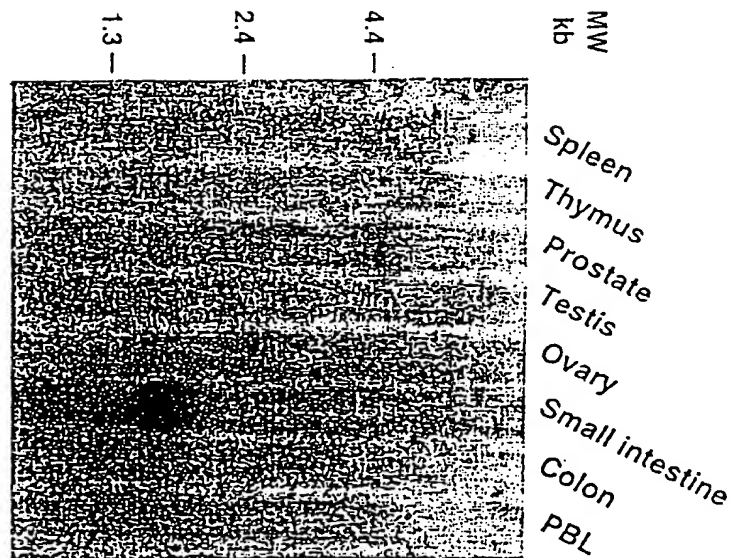


FIG. 4

8/11

09380546-11999

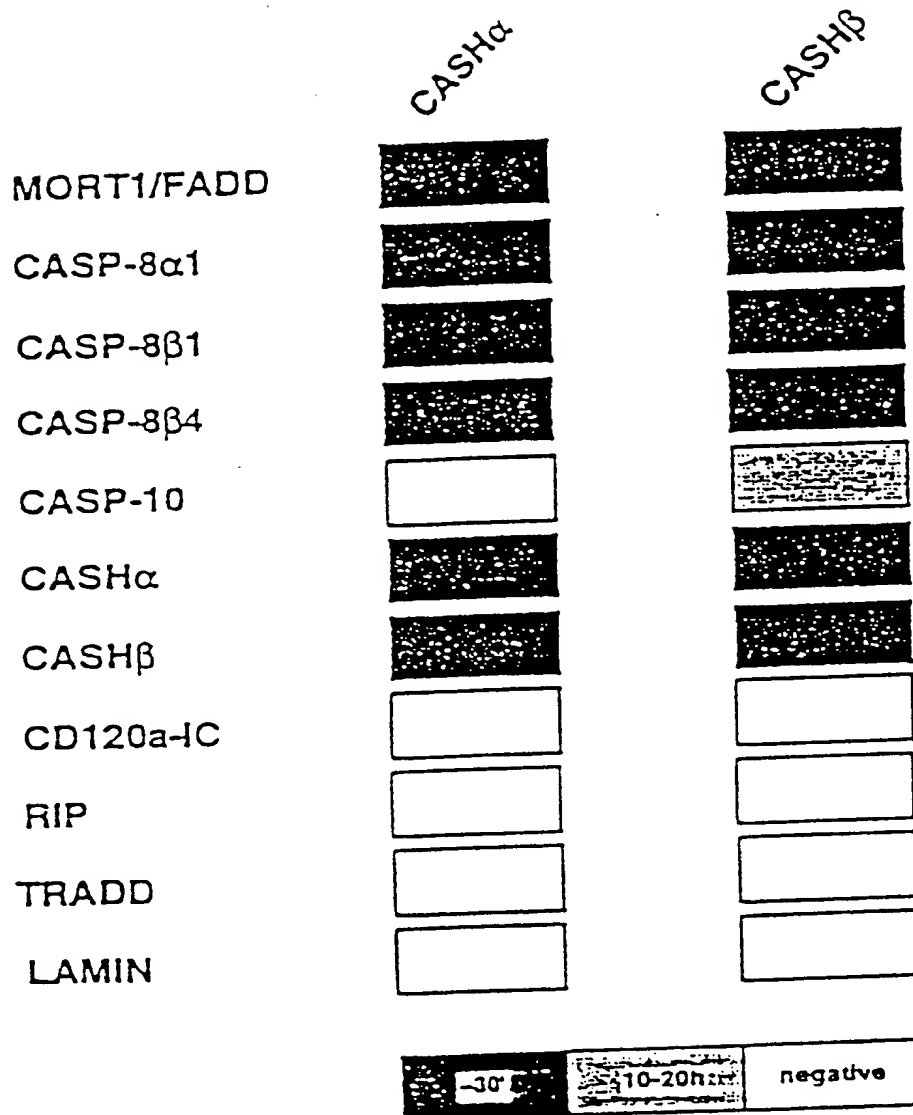


FIG. 5



9/11

# HeLa-Fas cells

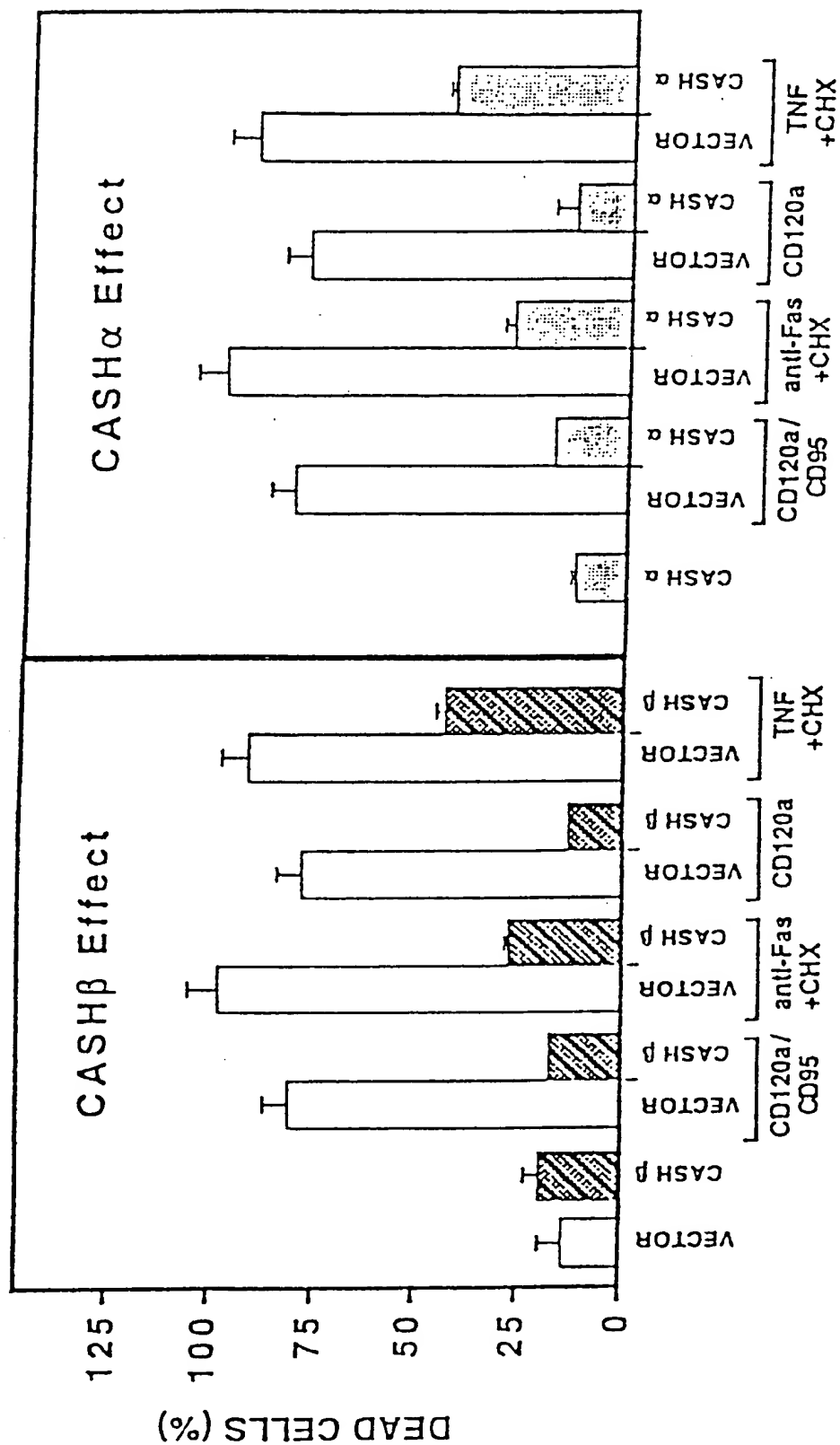


FIG. 6A

293-T cells

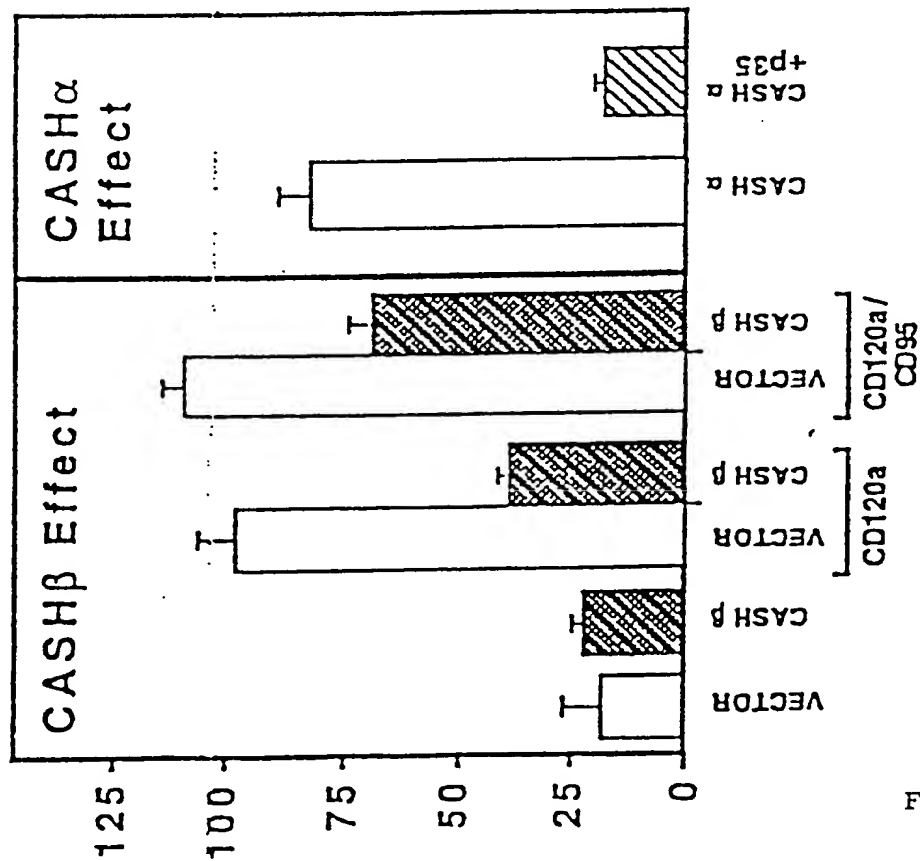


FIG. 6B

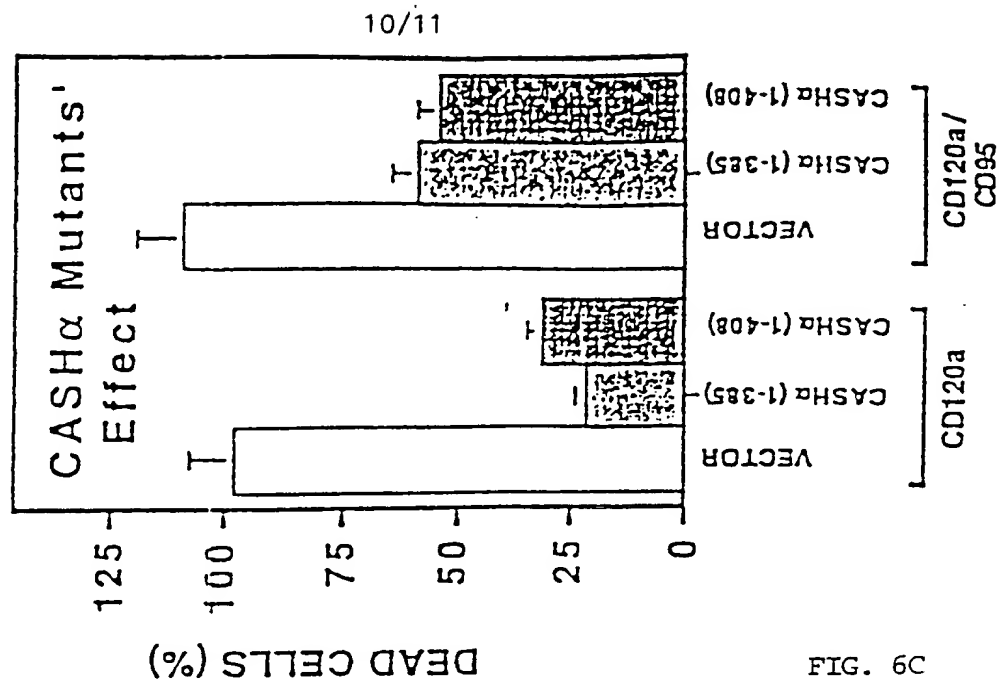
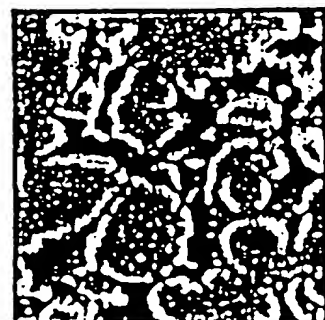


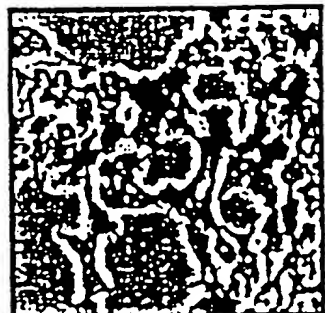
FIG. 6C

09380546

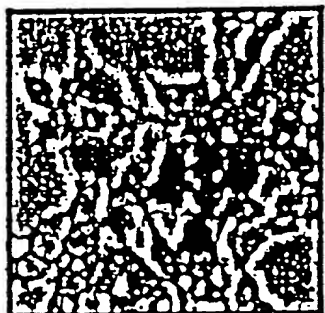
293-T cells



Vector



CASH  $\alpha$



CD120 a



CD120 a + CASH  $\alpha$  (1-4)

FIG. 6D